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RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/043,774A

DATE: 04/25/2002
TIME: 14:31:09

Input Set : N:\Crf3\04102002\J043774.raw
Output Set: N:\CRF3\04252002\J043774A.raw

1 <110> APPLICANT: University of Illinois at
2 <120> TITLE OF INVENTION: HUMAN HEMATOPOIETIC
3 <130> FILE REFERENCE: MBHB: CU08/PPA<160> 17 <170> PatentIn

ERRORED SEQUENCES

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MAY 08 2002

TECH CENTER 1603/2900

5 <210> SEQ ID NO: 1<211> 2328<212> DNA<213> Homo sapiens<220><221> CDS<222>

E--> 6 <211> LENGTH:

E--> 7 <212> TYPE:

W--> 8 <213> ORGANISM:

9 <223> OTHER INFORMATION: Human Hiwi Protein

W--> 0 <160> NUMBER OF SEQ ID NOS:

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13	1 5 10 15	
14	tca aaa aca ggt tct tca ggc att ata gta agg tta agc act aac cat	96
15	Ser Lys Thr Ser Ser Gly Ile Ile Val Arg Leu Ser Thr Asn His	
16	20 25 30	
17	ttc cgg ctg aca tcc cgt ccc cag tgg gcc tta tat cag tat cac att	144
18	Phe Arg Leu Thr Ser Arg Pro Gln Trp Ala Leu Tyr Gln Tyr His Ile	
19	35 40 45	
20	gac tat aac cca ctg atg gaa gcc aga aga ctc cgt tca gct ctt ctt	192
21	Asp Tyr Asn Pro Leu Met Glu Ala Arg Arg Leu Arg Ser Ala Leu Leu	
22	50 55 60	
23	ttt caa cac gaa gat cta att gga aag tgt cat gct ttt gat gga acg	240
24	Phe Gln His Glu Asp Leu Ile Gly Lys Cys His Ala Phe Asp Gly Thr	
25	65 70 75 80	
26	ata tta ttt tta cct aaa aga cta cag caa aag gtt act gaa gtt ttt	288
27	Ile Leu Phe Leu Pro Lys Arg Leu Gln Gln Lys Val Thr Glu Val Phe	
28	85 90 95	
29	att aag acc cgg aat gga gag gat gtg agg ata acg atc act tta aca	336
30	Ser Lys Thr Arg Asn Gly Glu Asp Val Arg Ile Thr Ile Leu Thr	
31	100 105 110	
32	aat gaa ctt cca cct aca tca cca act tgt ttg cag ttc tat aat att	384
33	Asn Glu Leu Pro Pro Thr Ser Pro Thr Cys Leu Gln Phe Tyr Asn Ile	
34	115 120 125	
35	att ttc agg agg ctt ttg aaa atc atg aat ttg caa caa att gga cga	432
36	Ile Phe Arg Arg Leu Leu Lys Ile Met Asn Leu Gln Gln Ile Gly Arg	
37	130 135 140	
38	aat tat tat aac cca aat gac cca att gat att cca agt cac agg ttg	480
39	Asn Tyr Tyr Asn Pro Asp Pro Ile Asp Ile Pro Ser His Arg Leu	

Sample page
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error. Please
Contact:
Robert WAX at:
703-306-4119 or
703-308-4214

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43	165	170	175		
44	atc atg ctc tgc act gac gtt agc cat aaa gtc ctt cga agt gag act				576
45	Ile Met Leu Cys Thr Asp Val Ser His Lys Val Leu Arg Ser Glu Thr				
46	180	185	190		
47	gtt ttg gat ttc atg ttc aac ttt tat cat cag aca gaa gaa cat aaa				624
48	Val Leu Asp Phe Met Phe Asn Phe Tyr His Gln Thr Glu Glu His Lys				
49	195	200	205		
50	ttt caa gaa caa gtt tcc aaa gaa cta ata ggt tta gtt gtt ctt acc				672
51	Phe Gln Glu Gln Val Ser Lys Glu Leu Ile Gly Leu Val Val Leu Thr				
52	210	215	220		
53	aag tat aac aat aag aca tac aga gtg gat gat att gac tgg gac cag				720
54	Lys Tyr Asn Asn Lys Thr Tyr Arg Val Asp Asp Ile Asp Trp Asp Gln				
55	225	230	235	240	
56	aat ccc aag agc acc ttt aag aaa gcc gac ggc tct gaa gtc agc ttc				768
57	Asn Pro Lys Ser Thr Phe Lys Lys Ala Asp Gly Ser Glu Val Ser Phe				
58	245	250	255		
59	tta gaa tac tac agg aag caa tac aac caa gag atc acc gac ttg aag				816
60	Leu Glu Tyr Tyr Arg Lys Gln Tyr Asn Gln Glu Ile Thr Asp Leu Lys				
61	260	265	270		
62	cag cct gtc ttg gtc agc cag ccc aag aga agg cgg ggc oct ggg ggg				864
63	Gln Pro Val Leu Val Ser Gln Pro Lys Arg Arg Gly Pro Gly Gly				
64	275	280	285		
65	aca ctg cca ggg cct gcc atg ctc att cct gag ctc tgc tat ctt aca				912
66	Thr Leu Pro Gly Pro Ala Met Leu Ile Pro Glu Leu Cys Tyr Leu Thr				
67	290	295	300		
68	ggt cta act gat aaa atg cgt aat gat ttt aac gtg atg aaa gac tta				960
69	Gly Leu Thr Asp Lys Met Arg Asn Asp Phe Asn Val Met Lys Asp Leu				
70	305	310	315	320	
71	gcc gtt cat aca aga cta act cca gag caa agg cag cgt gaa gtg gga				1008
72	Ala Val His Thr Arg Leu Thr Pro Glu Gln Arg Gln Arg Glu Val Gly				
73	325	330	335		
74	cga ctc att gat tac att cat aaa aac gat aat gtt caa agg gag ctt				1056
75	Arg Leu Ile Asp Tyr Ile His Lys Asn Asp Asn Val Gln Arg Glu Leu				
76	340	345	350		
77	cga gac tgg ggt ttg agc ttt gat tcc aac tta ctg tcc ttc tca gga				1104
78	Arg Asp Trp Gly Leu Ser Phe Asp Ser Asn Leu Leu Ser Phe Ser Gly				
79	355	360	365		
80	aga att ttg caa aca gaa aag att cac caa ggt gga aaa aca ttt gat				1152
81	Arg Ile Leu Gln Thr Glu Lys Ile His Gln Gly Gly Lys Thr Phe Asp				
82	370	375	380		
83	tac aat cca caa ttt gca gat tgg tcc aaa gaa aca aga ggt gca cca				1200
84	Tyr Asn Pro Gln Phe Ala Asp Trp Ser Lys Glu Thr Arg Gly Ala Pro				
85	385	390	395	400	
86	tta att agt gtt aag cca cta gat aac tgg ctg ttg atc tat acg cga				1248
87	Leu Ile Ser Val Lys Pro Leu Asp Asn Trp Leu Leu Ile Tyr Thr Arg				
88	405	410	415		

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89	aga aat tat gaa gca gcc aat tca ttg ata caa aat cta ttt aaa gtt	1296
90	Arg Asn Tyr Glu Ala Ala Asn Ser Leu Ile Gln Asn Leu Phe Lys Val	
91	420 425 430	
92	aca cca gcc atg ggc atg caa atg aga aaa gca ata atg att gaa gtg	1344
93	Thr Pro Ala Met Gly Met Gln Met Arg Lys Ala Ile Met Ile Glu Val	
94	435 440 445	
95	gat gac aga act gaa gcc tac tta aga gtc tta cag caa aag gtc aca	1392
96	Asp Asp Arg Thr Glu Ala Tyr Leu Arg Val Leu Gln Gln Lys Val Thr	
97	450 455 460	
98	gca gac acc cag ata gtt gtc tgt ctg ttg tca agt aat cgg aag gac	1440
99	Ala Asp Thr Gln Ile Val Val Cys Leu Leu Ser Ser Asn Arg Lys Asp	
100	465 470 475 480	
101	aaa tac gat gct att aaa aaa tac ctg tgt aca gat tgc cct acc cca	1488
102	Lys Tyr Asp Ala Ile Lys Lys Tyr Leu Cys Thr Asp Cys Pro Thr Pro	
103	485 490 495	
104	agt cag tgt gtg gtc cga acc tta ggc aaa cag caa act gtc atg	1536
105	Ser Gln Cys Val Val Ala Arg Thr Leu Gly Lys Gln Gln Thr Val Met	
106	500 505 510	
107	gcc att gct aca aag att gcc cta cag atg aac tgc aag atg gga gga	1584
108	Ala Ile Ala Thr Lys Ile Ala Leu Gln Met Asn Cys Lys Met Gly Gly	
109	515 520 525	
110	gag ctc tgg agg gtg gac atc ccc ctg aag ctc gtg atg atc gtt ggc	1632
111	Glu Leu Trp Arg Val Asp Ile Pro Leu Lys Leu Val Met Ile Val Gly	
112	530 535 540	
113	atc gat tgt tac cat gac atg aca gct ggg cgg agg tca atc gca gga	1680
114	Ile Asp Cys Tyr His Asp Met Thr Ala Gly Arg Arg Ser Ile Ala Gly	
115	545 550 555 560	
116	ttt gtt gcc agc atc aat gaa ggg atg acc cgc tgg ttc tca cgc tgc	1728
117	Phe Val Ala Ser Ile Asn Glu Gly Met Thr Arg Trp Phe Ser Arg Cys	
118	565 570 575	
119	ata ttt cag gat aga gga cag gag ctg gta gat ggg ctc aaa gtc tgc	1776
120	Ile Phe Gln Asp Arg Gly Gln Glu Leu Val Asp Gly Leu Lys Val Cys	
121	580 585 590	
122	ctg caa gcg gct ctg agg gct tgg aat agc tgc aat gag tac atg ccc	1824
123	Leu Gln Ala Ala Leu Arg Ala Trp Asn Ser Cys Asn Glu Tyr Met Pro	
124	595 600 605	
125	agc cgg atc atc gtg tac cgc gat ggc gta gga gac ggc cag ctg aaa	1872
126	Ser Arg Ile Ile Val Tyr Arg Asp Gly Val Gly Asp Gly Gln Leu Lys	
127	610 615 620	
128	aca ctg gtg aac tac gaa gtg cca cag ttt ttg gat tgt cta aaa tcc	1920
129	Thr Leu Val Asn Tyr Glu Val Pro Gln Phe Leu Asp Cys Leu Lys Ser	
130	625 630 635 640	
131	att ggt aga ggt tac aac cct aga cta acg gta att gtg gtg aag aaa	1968
132	Ile Gly Arg Gly Tyr Asn Pro Arg Leu Thr Val Ile Val Val Lys Lys	
133	645 650 655	
134	aga gtg aac acc aga ttt ttt gct cag tct gga gga aga ctt cag aat	2016
135	Arg Val Asn Thr Arg Phe Phe Ala Gln Ser Gly Gly Arg Leu Gln Asn	
136	660 665 670	
137	cca ctt cct gga aca gtt att gat gta gag gtt acc aga cca gaa tgg	2064

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140	tat gac ttt ttt atc gtg agc cag gct gtg aga agt ggt agt gtt tct		2112	
141	Tyr Asp Phe Phe Ile Val Ser Gln Ala Val Arg Ser Gly Ser Val Ser			
142	690	695	700	
143	ccc aca cat tac aat gtc atc tat gac aac agc ggc ctg aag cca gac		2160	
144	Pro Thr His Tyr Asn Val Ile Tyr Asp Asn Ser Gly Leu Lys Pro Asp			
145	705	710	715	720
146	cac ata cag cgc ttg acc tac aag ctg tgc cac atc tat tac aac tgg		2208	
147	His Ile Gln Arg Leu Thr Tyr Lys Leu Cys His Ile Tyr Tyr Asn Trp			
148	725	730	735	
149	cca ggt gtc att cgt gtt cct gct cct tgc cag tac gcc cac aag ctg		2256	
150	Pro Gly Val Ile Arg Val Pro Ala Pro Cys Gln Tyr Ala His Lys Leu			
151	740	745	750	
152	gct ttt ctt gtt ggc cag agt att cac aga gag cca aat ctg tca ctg		2304	
153	Ala Phe Leu Val Gly Gln Ser Ile His Arg Glu Pro Asn Leu Ser Leu			
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155	tca aac cgc ctt tac tac ctc taa		2328	
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167	20	25		30	
168	Phe Arg Leu Thr Ser Arg Pro Gln Trp Ala Leu Tyr Gln Tyr His Ile				
169	35	40		45	
170	Asp Tyr Asn Pro Leu Met Glu Ala Arg Arg Leu Arg Ser Ala Leu Leu				
171	50	55		60	
172	Phe Gln His Glu Asp Leu Ile Gly Lys Cys His Ala Phe Asp Gly Thr				
173	65	70		75	80
174	Ile Leu Phe Leu Pro Lys Arg Leu Gln Gln Lys Val Thr Glu Val Phe				
175	85	90		95	
176	Ser Lys Thr Arg Asn Gly Glu Asp Val Arg Ile Thr Ile Thr Leu Thr				
177	100	105		110	
178	Asn Glu Leu Pro Pro Thr Ser Pro Thr Cys Leu Gln Phe Tyr Asn Ile				
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180	Ile Phe Arg Arg Leu Leu Lys Ile Met Asn Leu Gln Gln Ile Gly Arg				
181	130	135		140	
182	Asn Tyr Tyr Asn Pro Asn Asp Pro Ile Asp Ile Pro Ser His Arg Leu				
183	145	150		155	160
184	Val Ile Trp Pro Gly Phe Thr Thr Ser Ile Leu Gln Tyr Glu Asn Ser				
185	165	170		175	
186	Ile Met Leu Cys Thr Asp Val Ser His Lys Val Leu Arg Ser Glu Thr				
187	180	185		190	

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188 Val Leu Asp Phe Met Phe Asn Phe Tyr His Gln Thr Glu Glu His Lys
189 195 200 205
190 Phe Gln Gln Glu Val Ser Lys Glu Leu Ile Gly Leu Val Val Leu Thr
191 210 215 220
192 Lys Tyr Asn Asn Lys Thr Tyr Arg Val Asp Asp Ile Asp Trp Asp Gln
193 225 230 235 240
194 Asn Pro Lys Ser Thr Phe Lys Lys Ala Asp Gly Ser Glu Val Ser Phe
195 245 250 255
196 Leu Glu Tyr Tyr Arg Lys Gln Tyr Asn Gln Glu Ile Thr Asp Leu Lys
197 260 265 270
198 Gln Pro Val Leu Val Ser Gln Pro Lys Arg Arg Gly Pro Gly Gly
199 275 280 285
200 Thr Leu Pro Gly Pro Ala Met Leu Ile Pro Glu Leu Cys Tyr Leu Thr
201 290 295 300
202 Gly Leu Thr Asp Lys Met Arg Asn Asp Phe Asn Val Met Lys Asp Leu
203 305 310 315 320
204 Ala Val His Thr Arg Leu Thr Pro Glu Gln Arg Gln Arg Glu Val Gly
205 325 330 335
206 Arg Leu Ile Asp Tyr Ile His Lys Asn Asp Asn Val Gln Arg Glu Leu
207 340 345 350
208 Arg Asp Trp Gly Leu Ser Phe Asp Ser Asn Leu Leu Ser Phe Ser Gly
209 355 360 365
210 Arg Ile Leu Gln Thr Glu Lys Ile His Gln Gly Gly Lys Thr Phe Asp
211 370 375 380
212 Tyr Asn Pro Gln Phe Ala Asp Trp Ser Lys Glu Thr Arg Gly Ala Pro
213 385 390 395 400
214 Leu Ile Ser Val Lys Pro Leu Asp Asn Trp Leu Leu Ile Tyr Thr Arg
215 405 410 415
216 Arg Asn Tyr Glu Ala Ala Asn Ser Leu Ile Gln Asn Leu Phe Lys Val
217 420 425 430
218 Thr Pro Ala Met Gly Met Gln Met Arg Lys Ala Ile Met Ile Glu Val
219 435 440 445
220 Asp Asp Arg Thr Glu Ala Tyr Leu Arg Val Leu Gln Gln Lys Val Thr
221 450 455 460
222 Ala Asp Thr Gln Ile Val Val Cys Leu Leu Ser Ser Asn Arg Lys Asp
223 465 470 475 480
224 Lys Tyr Asp Ala Ile Lys Lys Tyr Leu Cys Thr Asp Cys Pro Thr Pro
225 485 490 495
226 Ser Gln Cys Val Val Ala Arg Thr Leu Gly Lys Gln Gln Thr Val Met
227 500 505 510
228 Ala Ile Ala Thr Lys Ile Ala Leu Gln Met Asn Cys Lys Met Gly Gly
229 515 520 525
230 Glu Leu Trp Arg Val Asp Ile Pro Leu Lys Leu Val Met Ile Val Gly
231 530 535 540
232 Ile Asp Cys Tyr His Asp Met Thr Ala Gly Arg Arg Ser Ile Ala Gly
233 545 550 555 560
234 Phe Val Ala Ser Ile Asn Glu Gly Met Thr Arg Trp Phe Ser Arg Cys
235 565 570 575
236 Ile Phe Gln Asp Arg Gly Gln Glu Leu Val Asp Gly Leu Lys Val Cys

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237	580	585	590	
238	Leu Gln Ala Ala Leu Arg Ala Trp Asn Ser Cys Asn Glu Tyr Met Pro			
239	595	600	605	
240	Ser Arg Ile Ile Val Tyr Arg Asp Gly Val Gly Asp Gly Gln Leu Lys			
241	610	615	620	
242	Thr Leu Val Asn Tyr Glu Val Pro Gln Phe Leu Asp Cys Leu Lys Ser			
243	625	630	635	640
244	Ile Gly Arg Gly Tyr Asn Pro Arg Leu Thr Val Ile Val Val Lys Lys			
245	645	650	655	
246	Arg Val Asn Thr Arg Phe Phe Ala Gln Ser Gly Gly Arg Leu Gln Asn			
247	660	665	670	
248	Pro Leu Pro Gly Thr Val Ile Asp Val Glu Val Thr Arg Pro Glu Trp			
249	675	680	685	
250	Tyr Asp Phe Phe Ile Val Ser Gln Ala Val Arg Ser Gly Ser Val Ser			
251	690	695	700	
252	Pro Thr His Tyr Asn Val Ile Tyr Asp Asn Ser Gly Leu Lys Pro Asp			
253	705	710	715	720
254	His Ile Gln Arg Leu Thr Tyr Lys Leu Cys His Ile Tyr Tyr Asn Trp			
255	725	730	735	
256	Pro Gly Val Ile Arg Val Pro Ala Pro Cys Gln Tyr Ala His Lys Leu			
257	740	745	750	
258	Ala Phe Leu Val Gly Gln Ser Ile His Arg Glu Pro Asn Leu Ser Leu			
259	755	760	765	
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354 35 40 45
355 Ala Ser Arg Glu Arg Arg Ala Leu Glu Ala Pro Arg Arg Glu Gly
356 50 55 60
357 Gly Pro Pro Glu Arg Lys Pro Trp Gly Asp Gln Tyr Asp Tyr Leu Asn
358 65 70 75 80
359 Thr Arg Pro Val Glu Leu Val Ser Lys Lys Gly Thr Asp Gly Val Pro
360 85 90 95
361 Val Met Leu Gln Thr Asn Phe Phe Arg Leu Lys Thr Lys Pro Glu Trp
362 100 105 110
363 Arg Ile Val His Tyr His Val Glu Phe Glu Pro Ser Ile Glu Asn Pro
364 115 120 125
365 Arg Val Arg Met Gly Val Leu Ser Asn His Ala Asn Leu Leu Gly Ser
366 130 135 140
367 Gly Tyr Leu Phe Asp Gly Leu Gln Leu Phe Thr Thr Arg Lys Phe Glu
368 145 150 155 160
369 Gln Glu Ile Thr Val Leu Ser Gly Lys Ser Lys Leu Asp Ile Glu Tyr
370 165 170 175
371 Lys Ile Ser Ile Lys Phe Val Gly Phe Ile Ser Cys Ala Glu Pro Arg
372 180 185 190
373 Phe Leu Gln Val Leu Asn Leu Ile Leu Arg Arg Ser Met Lys Gly Leu
374 195 200 205
375 Asn Leu Glu Leu Val Gly Arg Asn Leu Phe Asp Pro Arg Ala Lys Ile
376 210 215 220
377 Glu Ile Arg Glu Phe Lys Met Glu Leu Trp Pro Gly Tyr Glu Thr Ser
378 225 230 235 240
379 Ile Arg Gln His Glu Lys Asp Ile Leu Leu Gly Thr Glu Ile Thr His
380 245 250 255
381 Lys Val Met Arg Thr Glu Thr Ile Tyr Asp Ile Met Arg Arg Cys Ser
382 260 265 270
383 His Asn Pro Ala Arg His Gln Asp Glu Val Arg Val Asn Val Leu Asp
384 275 280 285
385 Leu Ile Val Leu Thr Asp Tyr Asn Asn Arg Thr Tyr Arg Ile Asn Asp
386 290 295 300
387 Val Asp Phe Gly Gln Thr Pro Lys Ser Thr Phe Ser Cys Lys Gly Arg
388 305 310 315 320
389 Asp Ile Ser Phe Val Glu Tyr Tyr Leu Thr Lys Tyr Asn Ile Arg Ile
390 325 330 335
391 Arg Asp His Asn Gln Pro Leu Leu Ile Ser Lys Asn Arg Asp Lys Ala
392 340 345 350
393 Leu Lys Thr Asn Ala Ser Glu Leu Val Val Leu Ile Pro Glu Leu Cys
394 355 360 365

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Input Set : N:\Crf3\04102002\J043774.raw
Output Set: N:\CRF3\04252002\J043774A.raw

395 Arg Val Thr Gly Leu Asn Ala Glu Met Arg Ser Asn Phe Gln Leu Met
 396 370 375 380
 397 Arg Ala Met Ser Ser Tyr Thr Arg Met Asn Pro Lys Gln Arg Thr Asp
 398 385 390 395 400
 399 Arg Leu Arg Ala Phe Asn His Arg Leu Gln Asn Thr Pro Glu Ser Val
 400 405 410 415
 401 Lys Val Leu Arg Asp Trp Asn Met Glu Leu Asp Lys Asn Val Thr Glu
 402 420 425 430
 403 Val Gln Gly Arg Ile Ile Gly Gln Gln Asn Ile Val Phe His Asn Gly
 404 435 440 445
 405 Lys Val Pro Ala Gly Glu Asn Ala Asp Trp Gln Arg His Phe Arg Asp
 406 450 455 460
 407 Gln Arg Met Leu Thr Thr Pro Ser Asp Gly Leu Asp Arg Trp Ala Val
 408 465 470 475 480
 409 Ile Ala Pro Gln Arg Asn Ser His Glu Leu Arg Thr Leu Leu Asp Ser
 410 485 490 495
 411 Leu Tyr Arg Ala Ala Ser Gly Met Gly Leu Arg Ile Arg Ser Pro Gln
 412 500 505 510
 413 Glu Phe Ile Ile Tyr Asp Asp Arg Thr Gly Thr Tyr Val Arg Ala Met
 414 515 520 525
 415 Asp Asp Cys Val Arg Ser Asp Pro Lys Leu Ile Leu Cys Leu Val Pro
 416 530 535 540
 417 Asn Asp Asn Ala Glu Arg Tyr Ser Ser Ile Lys Lys Arg Gly Tyr Val
 418 545 550 555 560
 419 Asp Arg Ala Val Pro Thr Gln Val Val Thr Leu Lys Thr Thr Lys Lys
 420 565 570 575
 421 Pro Tyr Ser Leu Met Ser Ile Ala Thr Lys Ile Ala Ile Gln Leu Asn
 422 580 585 590
 423 Cys Lys Leu Gly Tyr Thr Pro Trp Met Ile Glu Leu Pro Leu Ser Gly
 424 595 600 605
 425 Leu Met Thr Ile Gly Phe Asp Ile Ala Lys Ser Thr Arg Asp Arg Lys
 426 610 615 620
 427 Arg Ala Tyr Gly Ala Leu Ile Ala Ser Met Asp Leu Gln Gln Asn Ser
 428 625 630 635 640
 429 Thr Tyr Phe Ser Thr Val Thr Glu Cys Ser Ala Phe Asp Val Leu Ala
 430 645 650 655
 431 Asn Thr Leu Trp Pro Met Ile Ala Lys Ala Leu Arg Gln Tyr Gln His
 432 660 665 670
 433 Glu His Arg Lys Leu Pro Ser Arg Ile Val Phe Tyr Arg Asp Gly Val
 434 675 680 685
 435 Ser Ser Gly Ser Leu Lys Gln Leu Phe Glu Phe Glu Val Lys Asp Ile
 436 690 695 700
 437 Ile Glu Lys Leu Lys Thr Glu Tyr Ala Arg Val Gln Leu Ser Pro Pro
 438 705 710 715 720
 439 Gln Leu Ala Tyr Ile Val Val Thr Arg Ser Met Asn Thr Arg Phe Phe
 440 725 730 735
 441 Leu Asn Gly Gln Asn Pro Pro Pro Gly Thr Ile Val Asp Asp Val Ile
 442 740 745 750
 443 Thr Leu Pro Glu Arg Tyr Asp Phe Tyr Leu Val Ser Gln Gln Val Arg

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/043,774A

DATE: 04/25/2002
TIME: 14:31:10

Input Set : N:\Crf3\04102002\J043774.raw
Output Set: N:\CRF3\04252002\J043774A.raw

```

444      755          760          765
445 Gln Gly Thr Val Ser Pro Thr Ser Tyr Asn Val Leu Tyr Ser Ser Met
446      770          775          780
447 Gly Leu Ser Pro Glu Lys Met Gln Lys Leu Thr Tyr Lys Met Cys His
448      785          790          795          800
449 Leu Tyr Tyr Asn Trp Ser Gly Thr Thr Arg Val Pro Ala Val Cys Gln
450          805          810          815
451 Tyr Ala Lys Lys Leu Ala Thr Leu Val Gly Thr Asn Leu His Ser Ile
452          820          825          830
453 Pro Gln Asn Ala Leu Glu Lys Lys Phe Tyr Tyr Leu
454          835          840
456 <210> SEQ ID NO: 14<211> 29<212> DNA<213> Artificial Sequence<220><223> CD34
W--> 457 hematopoietic cell cDNA forward primer
E--> 458 <211> LENGTH:
E--> 459 <212> TYPE:
W--> 460 <213> ORGANISM:
461 <400> SEQUENCE: 14
462 atgatctttg gtgtgaacac aaggcagaa
464 <210> SEQ ID NO: 15<211> 31<212> DNA<213> Artificial Sequence<220><223> CD34
29
W--> 465 hematopoietic cell cDNA reverse primer
E--> 466 <211> LENGTH:
E--> 467 <212> TYPE:
W--> 468 <213> ORGANISM:
469 <400> SEQUENCE: 15
470 gaggtagtaa aggccgtttg acagtgcacag a
31
472 <210> SEQ ID NO: 16<211> 24<212> DNA<213> Artificial Sequence<220><223> human hiwi
W--> 473 gene forward primer
E--> 474 <211> LENGTH:
E--> 475 <212> TYPE:
W--> 476 <213> ORGANISM:
477 <400> SEQUENCE: 16
478 cttgccagt acgcccacaa gctg
24
480 <210> SEQ ID NO: 17<211> 27<212> DNA<213> Artificial Sequence<220><223> human hiwi
W--> 481 gene reverse primer
E--> 482 <211> LENGTH:
E--> 483 <212> TYPE:
W--> 484 <213> ORGANISM:
485 <400> SEQUENCE: 17
486 cccccacccat ggtttagtg agcatcc
27

```

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 04/25/2002
PATENT APPLICATION: US/10/043,774A TIME: 14:31:11

Input Set : N:\Crf3\04102002\J043774.raw
Output Set: N:\CRF3\04252002\J043774A.raw

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:2; Line(s) 263
Seq#:3; Line(s) 271
Seq#:6; Line(s) 295
Seq#:7; Line(s) 303
Seq#:8; Line(s) 311
Seq#:9; Line(s) 319
Seq#:10; Line(s) 327
Seq#:11; Line(s) 335
Seq#:15; Line(s) 472
Seq#:16; Line(s) 480

VERIFICATION SUMMARY DATE: 04/25/2002
PATENT APPLICATION: US/10/043,774A TIME: 14:31:11

Input Set : N:\Crf3\04102002\J043774.raw
Output Set: N:\CRF3\04252002\J043774A.raw

L:6 M:210 E: (40) Invalid Number of Sequences, LENGTH:
L:7 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:8 M:201 W: Mandatory field data missing, <213> ORGANISM
L:0 M:282 W: Numeric Field Identifier Missing, <160> is required.
L:10 M:200 E: Mandatory Header Field missing, <220> not found for SEQ ID#:1
L:160 M:210 E: (40) Invalid Number of Sequences, LENGTH:
L:161 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:162 M:201 W: Mandatory field data missing, <213> ORGANISM
L:163 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:2 differs:1
L:264 M:259 W: Allowed number of lines exceeded, <210> SEQ ID NO
L:265 M:210 E: (40) Invalid Number of Sequences, LENGTH:
L:266 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:267 M:201 W: Mandatory field data missing, <213> ORGANISM
L:272 M:259 W: Allowed number of lines exceeded, <210> SEQ ID NO
L:273 M:210 E: (40) Invalid Number of Sequences, LENGTH:
L:274 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:275 M:201 W: Mandatory field data missing, <213> ORGANISM
L:280 M:259 W: Allowed number of lines exceeded, <210> SEQ ID NO
L:281 M:210 E: (40) Invalid Number of Sequences, LENGTH:
L:282 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:283 M:201 W: Mandatory field data missing, <213> ORGANISM
L:288 M:259 W: Allowed number of lines exceeded, <210> SEQ ID NO
L:289 M:210 E: (40) Invalid Number of Sequences, LENGTH:
L:290 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:291 M:201 W: Mandatory field data missing, <213> ORGANISM
L:296 M:259 W: Allowed number of lines exceeded, <210> SEQ ID NO
L:297 M:210 E: (40) Invalid Number of Sequences, LENGTH:
L:298 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:299 M:201 W: Mandatory field data missing, <213> ORGANISM
L:304 M:259 W: Allowed number of lines exceeded, <210> SEQ ID NO
L:305 M:210 E: (40) Invalid Number of Sequences, LENGTH:
L:306 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:307 M:201 W: Mandatory field data missing, <213> ORGANISM
L:312 M:259 W: Allowed number of lines exceeded, <210> SEQ ID NO
L:313 M:210 E: (40) Invalid Number of Sequences, LENGTH:
L:314 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:315 M:201 W: Mandatory field data missing, <213> ORGANISM
L:320 M:259 W: Allowed number of lines exceeded, <210> SEQ ID NO
L:321 M:210 E: (40) Invalid Number of Sequences, LENGTH:
L:322 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:323 M:201 W: Mandatory field data missing, <213> ORGANISM
L:328 M:259 W: Allowed number of lines exceeded, <210> SEQ ID NO
L:329 M:210 E: (40) Invalid Number of Sequences, LENGTH:
L:330 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:331 M:201 W: Mandatory field data missing, <213> ORGANISM
L:336 M:259 W: Allowed number of lines exceeded, <210> SEQ ID NO
L:337 M:210 E: (40) Invalid Number of Sequences, LENGTH:
L:338 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:

VERIFICATION SUMMARY
PATENT APPLICATION: US/10/043,774A

DATE: 04/25/2002
TIME: 14:31:11

Input Set : N:\Crf3\04102002\J043774.raw
Output Set: N:\CRF3\04252002\J043774A.raw

L:339 M:201 W: Mandatory field data missing, <213> ORGANISM
L:344 M:210 E: (40) Invalid Number of Sequences, LENGTH:
L:345 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:346 M:201 W: Mandatory field data missing, <213> ORGANISM
L:348 M:200 E: Mandatory Header Field missing, <220> not found for SEQ ID#:13
L:457 M:259 W: Allowed number of lines exceeded, <210> SEQ ID NO
L:458 M:210 E: (40) Invalid Number of Sequences, LENGTH:
L:459 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:460 M:201 W: Mandatory field data missing, <213> ORGANISM
L:465 M:259 W: Allowed number of lines exceeded, <210> SEQ ID NO
L:466 M:210 E: (40) Invalid Number of Sequences, LENGTH:
L:467 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:468 M:201 W: Mandatory field data missing, <213> ORGANISM
L:473 M:259 W: Allowed number of lines exceeded, <210> SEQ ID NO
L:474 M:210 E: (40) Invalid Number of Sequences, LENGTH:
L:475 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:476 M:201 W: Mandatory field data missing, <213> ORGANISM
L:481 M:259 W: Allowed number of lines exceeded, <210> SEQ ID NO
L:482 M:210 E: (40) Invalid Number of Sequences, LENGTH:
L:483 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:484 M:201 W: Mandatory field data missing, <213> ORGANISM
L:0 M:203 E: No. of Seq. differs, <160> Number Of Sequences:Input (0) Counted (17)

STATISTICS SUMMARY

PATENT APPLICATION: US/10/043,774A -

DATE: 04/25/2002

TIME: 14:31:11

Input Set : N:\Crf3\04102002\J043774.raw

Output Set: N:\CRF3\04252002\J043774A.raw

Application Serial Number: US/10/043,774A

Alpha or Numeric: Numeric

Application Class:

Application File Date: 03-29-2002

Art Unit: OIPE

Software Application:

Total Number of Sequences: 17

Total Nucleotides: 0

Total Amino Acids: 0

Number of Errors: 38

Number of Warnings: 32

Number of Corrections: 0

MESSAGE SUMMARY

200 E: 2 (Mandatory Header Field missing)

201 W: 17 (Mandatory field data missing)

203 E: 1 (No. of Seq. differs)

210 E: 17 ((40) Invalid Number of Sequences)

212 E: 1 ((34) Invalid or duplicate Sequence ID Number)

259 W: 14 (Allowed number of lines exceeded)

282 W: 1 (Numeric Field Identifier Missing)

310 E: 17 ((3) Wrong or Missing Sequence Type)